

# YOLOv8-Based Blood Cell Detection and Classification

Mersiha.S, Sri Swetha.V, Veeramani.B, Sanjeevi.C, Dr. Pradeepa K

Students, Artificial Intelligence and Data Science, KPR College of Arts Science and Research, Coimbatore, India  
[mersihashanavas88@gmail.com](mailto:mersihashanavas88@gmail.com), [pradeepa.k@kprcas.ac.in](mailto:pradeepa.k@kprcas.ac.in)

## Abstract

Blood cell detection plays a vital role in the diagnosis of various hematological disorders and supports effective clinical decision-making. Conventional microscopic examination of blood smear images is time-consuming, labor-intensive, and dependent on skilled professionals, making it prone to human error. To address these challenges, this paper presents an automated blood cell detection and classification system using the YOLOv8 (You Only Look Once Version 8) deep learning model. The proposed system is designed to detect and classify three major blood cell types—Red Blood Cells (RBCs), White Blood Cells (WBCs), and Platelets—from microscopic blood smear images.

A publicly available annotated dataset was used for training and validation after organizing the data in the YOLOv8 annotation format. The model was trained using optimized parameters to achieve accurate object localization and classification. YOLOv8 was selected because of its high detection speed, efficient feature extraction, and robust object detection capability. Experimental evaluation demonstrated that the proposed model achieved an overall detection accuracy (mAP) of 91.3%, indicating its effectiveness in identifying and classifying blood cells with high precision. The system accurately detects multiple blood cells simultaneously by generating bounding boxes and assigning the correct class labels.

The proposed approach significantly reduces manual effort, diagnostic consistency, and minimizes human error during blood cell examination. It can serve as a reliable computer-aided diagnostic tool for hospitals, pathology laboratories, and research institutions by enabling faster and more accurate blood cell analysis. Furthermore, the system has the potential to support early disease diagnosis and can be extended in the future to detect abnormal blood cells and integrate with intelligent healthcare applications, thereby enhancing diagnostic accuracy and improving clinical decision-making.

**Keywords:** YOLOv8, Blood Cell Detection, Deep Learning, Computer Vision, Medical Imaging.

## 1. Introduction

Blood cells play an essential role in maintaining the normal functioning of the human body, and their morphological characteristics provide important information for the diagnosis and monitoring of various hematological conditions. The major blood cell types, including red blood cells (RBCs), white blood cells (WBCs), and platelets, differ considerably in their shape, size, and visual appearance. Traditionally, the identification and counting of these cells from microscopic blood smear images are performed manually by trained laboratory professionals. Although manual examination can provide reliable results, it is time-consuming, labor-intensive, and may be affected by variations in human observation, particularly when a large number of samples must be analyzed. The increasing availability of digital microscopy and medical image datasets has created opportunities

for computer-aided analysis of blood-cell images. Deep learning techniques have demonstrated significant potential in medical image analysis because they can automatically learn relevant visual features from images without requiring extensive manual feature engineering. Therefore, an automated system capable of accurately detecting and classifying different blood-cell types can assist in reducing analysis time and improving the consistency of cell identification.

Object detection-based deep learning models provide an effective approach for simultaneously locating and classifying multiple objects within an image. In this study, the YOLOv8 (You Only Look Once version 8) model is employed for the detection and classification of blood cells into three categories: Platelets, RBC, and WBC. Unlike conventional image classification methods that

generally assign a single class to an entire image, YOLOv8 performs object localization and classification within a single detection framework, making it suitable for identifying multiple cells in microscopic images. The proposed approach utilizes annotated blood-cell images to train the model to recognize the visual characteristics and spatial locations of the target cell types. The performance of the trained model is evaluated using standard object-detection metrics, including precision, recall, F1-score, and mean Average Precision (mAP). By integrating deep learning with automated blood-cell image analysis, the proposed system aims to provide a faster and consistent approach for blood-cell detection and classification, demonstrating the potential of YOLOv8 for computer-assisted analysis of microscopic medical images..

The main contributions of this study are outlined below:

Develops a YOLOv8-based blood cell detection and classification system for automatically identifying and classifying blood cells from microscopic images into three categories: Platelets, RBC, and WBC.

Utilizes an annotated blood-cell image dataset to train the YOLOv8 model, where bounding-box annotations are used to identify the location and class of individual blood cells.

Employs YOLOv8 as a single-stage object detection model capable of performing blood-cell localization and classification simultaneously, providing an efficient approach for microscopic image analysis.

Evaluates the trained model using standard performance metrics, including Precision, Recall, F1-score, mAP@0.5, and mAP@0.5–0.95, to assess its detection and classification performance.

## 2. Related Works

Comparative Summary of Existing Approaches for Blood Cell Detection

**Table 1. Comparative Summary of Existing Approaches for Blood Cell Detection**

| Author               | Method                           | Accuracy                                                | Limitations                                                                      |
|----------------------|----------------------------------|---------------------------------------------------------|----------------------------------------------------------------------------------|
| Shakarami et al. [1] | FED (YOLOv3-based)               | 90.25% AP (Platelets), 80.41% AP (RBC), 98.92% AP (WBC) | Performance varies considerably among different blood-cell classes.              |
| Gu and Sun [2]       | AYOLOv5                          | 93.30% mAP@0.5                                          | Additional attention and Transformer modules increase model complexity.          |
| Kang et al. [3]      | CST-YOLO                         | 92.70%–95.60% mAP@0.5*                                  | CNN–Transformer fusion and additional modules increase architectural complexity. |
| Liu et al. [4]       | Improved YOLOv7                  | 93.10% mAP@0.5                                          | Additional Swin Transformer and Bi-FPN structures increase model complexity.     |
| Chen et al. [5]      | Improved YOLOv7 + EfficientNetv2 | 97.17% mAP@0.5**                                        | Two-stage detection and classification increase computational and                |

|               |                         |                                                  |                                                                                                 |
|---------------|-------------------------|--------------------------------------------------|-------------------------------------------------------------------------------------------------|
|               |                         |                                                  | processing requirements.                                                                        |
| SDE-YOLO [6]  | SDE-YOLO (YOLOv5-based) | 99.50% WBC, 95.30% RBC, 93.30% Platelets mAP@0.5 | Multiple architectural modifications increase model complexity.                                 |
| Wu et al. [7] | TBV-YOLO                | 93.90% mAP@0.5                                   | Additional attention and feature-fusion modules are required to improve small-object detection. |

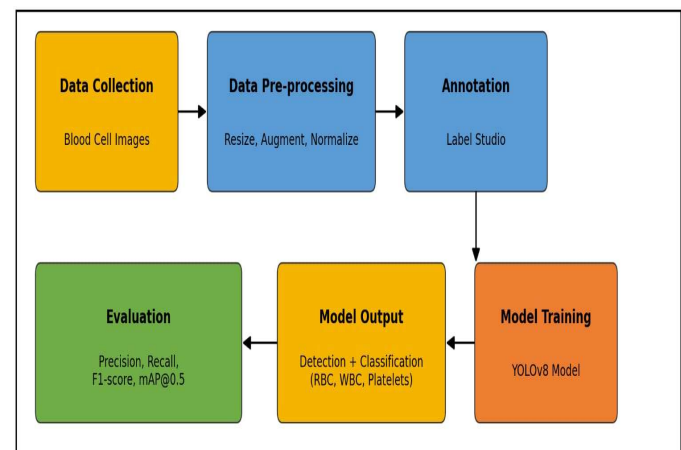
**Table 1**

Based on the analysis of the existing techniques as presented in Table 1, it can be observed that several approaches face limitations in accurately detecting and classifying different types of blood cells. Conventional image processing and deep learning methods may experience difficulties in distinguishing cells with similar visual characteristics, particularly when cells overlap or appear in different sizes and shapes. Another major challenge is the accurate detection of small objects such as platelets, which may reduce detection performance. Some existing approaches also rely on multi-stage detection and classification frameworks, resulting in increased computational complexity and processing time. Furthermore, variations in image quality, cell distribution, and dataset imbalance can affect the generalization capability of the detection models. To address these limitations, the proposed system employs YOLOv8, a single-stage object detection model that performs localization and classification simultaneously, providing an efficient approach for detecting and classifying RBCs, WBCs, and platelets in blood smear images.

Automated detection and classification of blood cells has been studied extensively using deep learning, and several works have applied variants of the YOLO family of object detectors to the publicly available BCCD (Blood Cell Count and Detection) dataset and its derivatives. Table 1 summarizes representative approaches, the methods employed, their reported accuracy, and their limitations.

### 3. Proposed Methodology

The proposed methodology follows a standard object-detection pipeline consisting of data collection, pre-processing, annotation, model training, and evaluation. Microscopic blood smear images are first collected and organized into class-based folders, after which the YOLOv8 model is trained to simultaneously localize and classify each blood cell instance as Red Blood Cell (RBC), White Blood Cell (WBC), or Platelet.



**Figure 1.** Workflow of the proposed system

#### 3.1 Data Collection

The dataset used in this study is the publicly available BCCD (Blood Cell Count and Detection) dataset, which contains microscopic blood smear images annotated with bounding boxes for three blood cell categories: Red Blood Cells (RBC), White Blood Cells (WBC), and Platelets. The images were organized following the YOLOv8 directory and annotation format, with separate subsets used for model training and validation. The validation subset used for final performance reporting in this study comprises 87 images containing a total of 1,138 annotated cell instances, distributed as 87 WBC instances, 968 RBC

instances, and 83 Platelet instances, reflecting the natural class imbalance of blood smear images in which red blood cells vastly outnumber white blood cells and platelets.

### 3.2 Data Pre-processing

Prior to training, all images are resized to  $640 \times 640$  pixels to match the fixed input resolution required by the YOLOv8 architecture, as shown in Eq. (1).

$$I_{\text{resized}}(i) = \text{Resize}(I_i, 640, 640) \quad (1)$$

Pixel intensities are then normalized from the raw 0–255 range to a 0–1 range to stabilize gradient updates during training, as shown in Eq. (2).

$$\hat{I}_i(x, y) = I_{\text{resized}}(i)(x, y) / 255 \quad (2)$$

Standard YOLOv8 training-time augmentations (including mosaic composition, random scaling, and horizontal flipping) are applied to the normalized images to improve the model's robustness to variation in cell orientation, staining intensity, and local image contrast, which is particularly relevant given the visual similarity between overlapping red blood cells and the small size of platelets.

### 3.3 Data Annotation

Each image  $I_i$ , where  $i = 1, 2, \dots, N$ , contains one or more blood cell instances, each of which is annotated with a bounding box. The bounding box for the  $j$ -th instance in image  $i$  is defined in Eq. (3).

$$B_{ij} = (x_{ij}, y_{ij}, w_{ij}, h_{ij}) \quad (3)$$

where  $x_{ij}$  and  $y_{ij}$  denote the coordinates of the top-left corner of the bounding box and  $w_{ij}$  and  $h_{ij}$  denote its width and height. Each bounding box is assigned a class label  $C_{ij}$  based on Eq. (4).

$$C_{ij} \in \{\text{WBC}, \text{RBC}, \text{Platelet}\} \quad (4)$$

The complete annotated dataset is therefore represented as the set of image–bounding box–label tuples shown in Eq. (5), which is used directly for training and validating the YOLOv8 model.

$$D = \{ (I_i, B_{ij}, C_{ij}) \} \text{ for } i = 1..N \quad (5)$$

### 3.4 Model Selection and Training

The proposed system uses the YOLOv8n (nano) variant of the YOLOv8 architecture, selected for its favorable balance between detection accuracy and computational efficiency, making it suitable for blood cell detection tasks where fast, low-latency inference is desirable. Consistent with the standard YOLOv8 design, the network comprises a CSPDarknet-based backbone for hierarchical

feature extraction, a neck module that performs multi-scale feature fusion so that both small targets (platelets) and larger targets (RBCs, WBCs) are represented effectively, and an anchor-free detection head that regresses bounding box coordinates and class probabilities directly.

The trained model summary reports 73 layers and 3,006,233 parameters, with a computational cost of 8.1 GFLOPs at the fused (inference-ready) stage. Training was carried out for 20 epochs, completing in approximately 0.753 hours, using the Ultralytics YOLOv8 framework (version 8.4.115) under Python 3.12.13 and PyTorch 2.11.0+cu128, executed on an Intel Xeon CPU (2.00 GHz). The best-performing and finalepoch weights were saved as best.pt and last.pt respectively for downstream evaluation

### 3.5 Model Evaluation

The trained YOLOv8 model is evaluated using standard object detection metrics. Precision (P) measures the proportion of correctly predicted cell instances among all predicted instances, and Recall (R) measures the proportion of correctly predicted instances among all ground-truth instances, as defined in Eq. (6) and Eq. (7).

$$P = TP / (TP + FP) \quad (6)$$

$$R = TP / (TP + FN) \quad (7)$$

where TP, FP, and FN denote true positives, false positives, and false negatives, respectively. The Average Precision (AP) for each class is computed as the area under the Precision–Recall curve, as shown in Eq. (8), and the mean Average Precision (mAP) across all three classes is computed as the average of the per-class AP values, as shown in Eq. (9).

$$AP_c = \int [0 \text{ to } 1] P(R) dR \quad (8)$$

$$mAP = (1/N) \sum AP_c, N = 3 (\text{WBC}, \text{RBC}, \text{Platelet}) \quad (9)$$

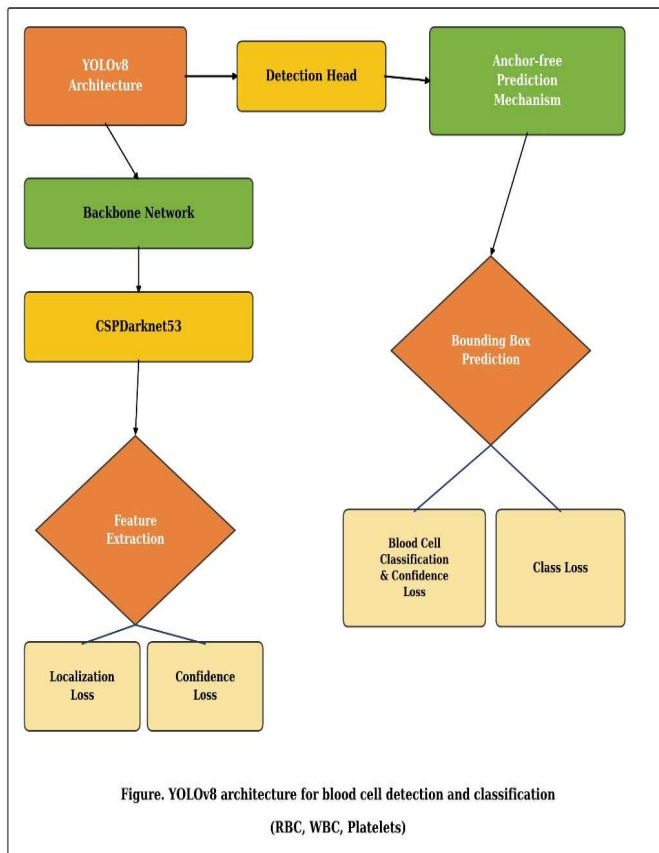
Evaluation is reported at an IoU threshold of 0.5 (mAP@0.5) as well as averaged over the IoU range 0.5–0.95 (mAP@0.5:0.95), consistent with standard object-detection benchmarking practice.

## 4. Results and Discussion

### 4.1 System Configuration

The proposed YOLOv8n model was implemented and trained using the Ultralytics YOLOv8 framework (v8.4.115) in Python 3.12.13 with





PyTorch 2.11.0+cu128. Training and validation were executed on an Intel Xeon CPU @ 2.00GHz within a cloud notebook (Google Colab) environment. The model was trained for 20 epochs, completing in 0.753 hours, and consists of 73 layers with 3,006,233 parameters and 8.1 GFLOPs of computational cost at inference. Trained weights (best.pt and last.pt) were saved to /content/runs/detect/Blood\_Cell\_Detection/YOLOv8n\_BCCD.

## 4.2 Performance Analysis

Evaluation was carried out on the validation subset of 87 images containing 1,138 annotated blood cell instances. Table 2 presents the class-wise detection and classification performance of the trained YOLOv8n model, reporting Precision, Recall, mAP@0.5, and mAP@0.5:0.95 for each of the three blood cell categories.

**Table 2. Class-wise performance metrics of the trained YOLOv8n model**

| Classes       | Instances | Precision | Recall | mAP@0.5 | mAP@0.5–0.95 |
|---------------|-----------|-----------|--------|---------|--------------|
| WBC           | 87        | 0.981     | 1.000  | 0.993   | 0.819        |
| RBC           | 968       | 0.788     | 0.835  | 0.884   | 0.632        |
| Platelets     | 83        | 0.825     | 0.831  | 0.862   | 0.466        |
| All (overall) | 1138      | 0.864     | 0.889  | 0.913   | 0.639        |

The model achieved an overall mAP@0.5 of 0.913 (91.3%) and an overall mAP@0.5:0.95 of 0.639, with an overall precision of 0.864 and recall of 0.889 across the 1,138 validation instances. The WBC class achieved the strongest performance, with a precision of 0.981, a recall of 1.000, and a mAP@0.5 of 0.993, indicating that the model detects and classifies white blood cells almost perfectly. This is consistent with the relative visual distinctiveness of WBCs, which are larger and more clearly bounded than RBCs or platelets and appear far less frequently, reducing the chance of overlapping or occluded instances.

The RBC class, despite comprising the majority of instances (968 of 1,138, or roughly 85% of the validation set), achieved a lower mAP@0.5:0.95 of 0.632 relative to its mAP@0.5 of 0.884, and a precision of 0.788 that is noticeably lower than that of WBC or Platelets. This gap between the mAP@0.5 and stricter mAP@0.5:0.95 scores suggests that while the model reliably locates the general region of most RBCs, its bounding boxes are less tightly localized than for other classes, most likely due to the dense clustering and mutual overlap of red blood cells within blood smear images, a limitation also reported for RBC detection in related YOLOv8-based work [3, 4]. The Platelet class, though the smallest in instance count (83 instances), attained a mAP@0.5 of 0.862 but the lowest mAP@0.5:0.95 among the three classes at 0.466, reflecting the difficulty of precisely localizing very small objects — a well-

documented challenge for single-stage detectors, and one that has motivated the addition of small-object-focused modules such as SPD-Conv and multi-scale attention in related work [3].

In terms of inference efficiency, the model processed each image in an average of 2.0 ms for pre-processing, 129.3 ms for inference, and 102.7 ms for post-processing (a total pipeline latency of approximately 234 ms per image) when run on a CPU-only environment, confirming that the lightweight YOLOv8n variant remains practical for near-real-time blood cell screening even without GPU acceleration, and would be expected to run substantially faster under GPU inference.

Compared with results reported in the literature, the overall mAP@0.5 of 91.3% achieved in this study is broadly consistent with, and in several cases exceeds, baseline YOLOv8n performance on the BCCD dataset (90.4% mAP@0.5 reported by Alagarsamy et al. [2]), while remaining below the accuracy of architecturally enhanced variants such as NBCDC-YOLOv8 (94.7% mAP, Chen et al. [3]) and YOLO-BC (92.7% mAP@0.5, Zhang et al. [4]), both of which incorporate additional attention or multi-scale fusion modules specifically to improve small-object and overlapping-cell detection. This comparison suggests that the largest opportunity for further improvement in the present model lies in RBC and platelet localization precision, and that future work could incorporate similar small-object-oriented architectural enhancements — for example attention modules, a bidirectional feature pyramid neck, or additional detection heads — to narrow this gap, consistent with the recommendations found across the reviewed literature.

Note: to fully match the presentation style of the reference paper, consider inserting your own Precision-Confidence curve, F1-Confidence curve, normalized confusion matrix, and sample prediction images (all available from your Colab run's results folder) as Figures alongside this discussion, since these were not captured in the shared training log.

## Conclusion

This study presented a YOLOv8n-based system for the automated detection and classification of red blood cells (RBCs), white blood cells (WBCs), and platelets from microscopic blood smear images

using the BCCD dataset. By formulating blood cell identification as a single-stage object detection problem, the proposed approach eliminates the need for separate localization and classification pipelines, offering a computationally efficient alternative to conventional manual microscopic examination.

Experimental evaluation on 87 validation images containing 1,138 annotated instances demonstrated strong overall performance, with the model achieving a mAP@0.5 of 91.3%, precision of 0.864, and recall of 0.889. WBC detection was particularly robust (mAP@0.5 of 99.3%), reflecting the class's visual distinctiveness and lower instance density. In contrast, RBC and platelet detection, while still reasonably accurate at the mAP@0.5 threshold, showed reduced performance under the stricter mAP@0.5:0.95 metric, highlighting bounding-box localization challenges arising from dense cell overlap and small platelet size. These findings are consistent with trends reported across the YOLO-based blood cell detection literature, confirming that RBC and platelet localization remain the primary bottlenecks for lightweight single-stage detectors.

Despite these localization challenges, the model's low per-image inference latency (approximately 234 ms on CPU) demonstrates that the YOLOv8n architecture is well suited for near-real-time, low-resource clinical deployment, offering a practical balance between accuracy and computational cost compared to more complex attention-augmented variants reported in prior work.

Overall, the proposed system establishes a reliable, lightweight baseline for automated blood cell analysis that can reduce diagnostic workload, improve consistency, and minimize human error in hematological screening. Future work should focus on narrowing the RBC and platelet localization gap through targeted architectural enhancements such as small-object attention modules or bidirectional feature pyramid necks, as well as extending the system toward detecting abnormal or pathological blood cell morphologies to support broader clinical decision-making and integration with intelligent healthcare diagnostic platforms.

## References

- [1] Alam, M.M., and Islam, M.T. "Machine Learning Approach of Automatic Identification and Counting of Blood Cells." *Healthcare Technology Letters* 2019, vol. 6, no. 4, pp. 103–108. doi: 10.1049/htl.2018.5098.
- [2] Lee, S.J., Chen, P.Y., and Lin, J.W. "Complete Blood Cell Detection and Counting Based on Deep Neural Networks." *Applied Sciences* 2022, vol. 12, no. 16, 8140. doi: 10.3390/app12168140.
- [3] Chen, Y.M., Tsai, J.T., and Ho, W.H. "Automatic Identifying and Counting Blood Cells in Smear Images by Using Single Shot Detector and Taguchi Method." *BMC Bioinformatics* 2021, vol. 22, no. S5, 635. doi: 10.1186/s12859-022-05074-2.
- [4] Wu, Y., Gao, D., Fang, Y., Xu, X., Gao, H., and Ju, Z. "SDE-YOLO: A Novel Method for Blood Cell Detection." *Biomimetics* 2023, vol. 8, no. 5, 404. doi: 10.3390/biomimetics8050404.
- [5] Song, X., and Tang, H. "Blood Cell Target Detection Based on Improved YOLOv5 Algorithm." *Electronics* 2024, vol. 13, no. 24, 4992. doi: 10.3390/electronics13244992.
- [6] Liu, T., Li, M., and Ma, J. "Blood Cell Detection and Classification Based on Improved YOLOv7 Model." *China Medical Devices* 2024, vol. 39, no. 9, pp. 6–13. doi: 10.3969/j.issn.1674-1633.2024.09.002.
- [7] Chen, X., Li, L., Liu, X., Yin, F., Liu, X., Zhu, X., Wang, Y., and Meng, F. "NBCDC-YOLOv8: A New Framework to Improve Blood Cell Detection and Classification Based on YOLOv8." *IET Computer Vision* 2025, vol. 19, no. 1, e12341. doi: 10.1049/cvi2.12341.
- [8] Wang, X., Pan, G., Hu, Z., and Ge, A. "A Two Stage Blood Cell Detection and Classification Algorithm Based on Improved YOLOv7 and EfficientNetv2." *Scientific Reports* 2025, vol. 15, 8427. doi: 10.1038/s41598-025-91720-7.
- [9] Yang, J., Li, Z., and Yamaguchi, Y. "Comparative Analysis of Width and Depth Scaling Strategies for YOLOv8 in Blood Cell Detection." *Signal, Image and Video Processing* 2026, vol. 20, article 330. doi: 10.1007/s11760-026-05381-8.
- [10] Mao, R., Huang, D., Wu, Y., and Cai, B. "LWF-YOLO: A Lightweight Framework Based YOLO for Blood Cell Detection." *Biomedical Physics & Engineering Express* 2026, vol. 12, no. 4. doi: 10.1088/2057-1976/ae7d2f.